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tggcaggccttcaaGAATGATGCCAC-GAaaTCATCCccGagCTcgGaGAGTACCCcGAGC
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LEngth-factor = 0
Matching-weight = 1
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US-10-788-606-11
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US-10-788-		US-10-788-	643
US-10-788-		US-10-788-	675
US-10-788-	428 TAGTGGGCCCGACTTCCGCTGCACCCCACCGCGCGCGCAGCGCGGGGCGTGCTG	US-10-788-	733 AA
consensus	gag-GGgCCcGacTTCCGCTGCATCCCcGAcCGCTACCGCGCGCGCGCGGGGGGGCGCTGcTG	US-10-788-	733 AA
US-10-788-	351 TGECCEGGGGGGGGGGGGGGGGGGAAGGTGGGGCTGGTGGCTCGTGCAAGTGCA	consensus	aa
US-10-788-		US-10-788-	533
US-10-788-	442 TGLCCCGGLGGLGCCGCGCGCGCGCGCAAGTGCGCTTGTTGCAAGTGCA	US-10-788-	639
US-10-788-	474 TGCCCCGGCGCGCCCCGCCCCCGCAAGTGCGCCTTGGTGGCCTCGTGCAAGTGCA	US-10-788-	643
US-10-788-	489 TGTCCCGGTGGTGAGGCGCCGCGCGCGCGCAAGTGCGCCTGGTGGCCCTCGTGCAAGTGCA	US-10-788-	675
US-10-788-	489 TGTCCCGGTGGTGAGGCGCCGCGCGCAAGGTGCGCCTGGTGGCCTCGTGCAAGTGCA	US-10-788-	794 TG
consensus	TGLCCcGGLGG-GcgCGCCGCGCGCAAGGTGCGcCTGGTGGCCTCGTGCAAGTGCA	US-10-788-	794 TG
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US-10-788-	503 AGCGCTCACCGCTTCCACAACCAGTCGGAGCTCAAGGACTTCGGCCCCGAGGCCGCCC	US-10-788-	639
US-10-788-	535 AGGCCTCACCCGCTTCCACAACCAGTCGGAGCTCAGGACTTCGGACCCGGAGCCGCGCG	US-10-788-	643
US-10-788-	550 AGCGCCTCACCCGCTTCCACAACCAGTCGGAGCTCAAGGACTTCGGGACCGAGGCCGCTCG	. US-10-788-	675
US-10-788-	550 AGGCCCTCACCCGCTTCCACAACCAGTCGGAGCTCAAGGACTTCGGGACCGAGGCCGCTCG	US-10-788-	855 CA
consensus	AGGGCCTCACCCGCTTCCACAACCAGTCGGAGCTCAAGGACTTCGGGcCcGAGGCCGC-CG	US-10-788-	855 CA
US-10-788-	473 GCCGCAAACGGGCCGGAAAGCEGCGGCCCCGGGGGACCAAAAGCCAAGCCAGGCGA	consensus	ຜ
US-10-788-		US-10-788-	533
US-10-788-	564 GCCGCNGAACGGCCGGAAGCCGCGCGCCCCGGGGGCCCAAAGCCAALCAGGCCGAG	US-10-788-	639
US-10-788-	596 GCCGCAGAAGGGCCGCGCCCCCGGGGGGCCCAAAGCCAACCAGGGGAG	US-10-788-	643
US-10-788-	611 GCCGCAGAAGGCCGGAAGCCGCGCCCCGGGCCCAAAGCCCAACCCGGGCGGG	US-10-788-	675
US-10-788-	611 GCCCCAGAAGGCCGCGCGCGCCCCCGCGAGCCCCAAAGCCAACCAGGCCCGAG	US-10-788-	916 CA
consensus	GCCGCAgAaGGGcCGgAAGCcGCGCCCCGCGCCCGGGGCGCCAAAGCCAacCaGGCcGAg	US-10-788-	916 CA
US-10-788-	. 533	consensus	α U
US-10-788-	619 CTGGAGAACGCCTACTAGag	US-10-788-	533
US-10-788-	625 CTGGAQAACGCCTACTAG	US-10-788-	639
US-10-788-	657 CTGGAACGCTACTAG	US-10-788-	643
US-10-788-	672 CTGGAGAACGCCTACTAGAGCCCGCGCCCCCCCCCCCCGGCGGGCG	US-10-788-	675
US-10-788-	672 CTGGAGAACGCCTACTAGAGCCCGCCCCCCCCCCCCCCC	US-10-788-	977 AG
consensus	ctggagaacgcctactagagcccgcccgccctccccaccggcgggcg	US-10-788-	977 AG
US-10-788-	533	consensus	8 D
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US-10-788-	675	
US-10-788-	733	AACCGCGCCCCACATTTCTGTCCTCTGCGCGTGGTTTGATTGTTTATATTTCATTGTAAA
US-10-788-	733	TTGATTGTTTATATTT
consensus		aacccgcgcccacatttctgtcctcgcgcgtggtttgattgtttatatttcattgtaaa
US-10-788-	533	
US-10-788-	639	
US-10-788-	643	
US-10-788-	675	
US-10-788-	794	TGCCTGCAACCCAGGGGGGTGAGACCTTCCAGGCCCTGAGGAATCCCGGGCGCGG
US-10-788-	794	GGGCAGGGGCTGAGACCTTCCAGGC
consensus		tgcctgcaacccagggcagggggttgagaccttccaggccctgaggaatcccggggcgccgg
US-10-788-	533	
US-10-788-	639	
US-10-788-	643	
US-10-788-	675	
US-10-788-	855	CAAGGCCCCCTCAGCCCGCCAGCTGAGGGGTCCCACGGGGCAGGGAATTGAGAGT
US-10-788-	855	
consensus		caaggccccctcagcccgccagctgaggggtcccacgggggaggga
US-10-788-	533	
US-10-788-	639	
US-10-788-	643	
US-10-788-	675	
US-10-788-	916	CACAGACACTAGCCACGCAGCCCCCTCTGGGGCCCCTACCTTTGCTGGTCCCACTTC
US-10-788-	916	CACAGACACTGAGCCACGCCCCGCCTCTGGGGCCGCCTACCTTTGCTGGTCCCTTTC
consensus		cacagacactgagccacgcagccccgcctctggggccgcctacctttgctggtcccacttc
US-10-788-	533	
US-10-788-	639	
US-10-788-	643	
US-10-788-	675	
US-10-788-	977	AGAGGAGGCAGAAATGGAAGCATTTTCACCGCCCTGGGGTTTTAAAGGAGCGGTGTGGGAG
US-10-788-	977	AGAGGAGGCAGAAATGGAAGCATTTTCACCGCCCTGGGGTTTTAAGGGAGCGGTGTGGGAA
consensus		agaggaggcagaaatggaagcattttcaccgccctggggttttaagggagcggtgtgggag

US-10-788- 533		US-10-788- 643	- 675 - 1343 AAAGAGAGAGAATGAATGCATTGCATTGATTCAGTGCCAAGGTCACTTC	US-10-788- 1343 AAAGAGAGAATGAATGCAGTTGCATTGATTCAGTGCCAAGGTCACTTCCAGAATTCAGA consensus aaagagagaatgaatgcagttgcattgattcagtgccaaggtcacttccagaattcaga	US-10-788- 533	US-10-788- 639	US-10-788- 643	US-10-788- 675 US-10-788- 1404 GTHGTGANGCTCTCTTGACGCCAAAGATGAAAAAAAAAAAAAA	US-10-788- 1404 GTTGTGATGCTCTTCTGACAGCCAAGATGAAAAAAAAAA	consensus gttgtgatgctcttctgacagccaaagatgaaaaacaaaaaaaa	US-10-788- 533	US-10-788- 639	US-10-788- 643	US-10-788- 675	US-10-788- 1465 GTCTATTTATGGCTGACATATTTACGGCTGACAAAACTCCTGGAAGAAGCTATGCTGCTTCC	CTGACAACTCCTGGAAGAAGCTATG	consensus gtctatttatggctgacatatttacggctgacaaactcctggaagaagctatgctgctcc	US-10-788- 533	US-10-788- 639	US-10-788- 643	US-10-788- 675		US-10-788- 1526 CAGCCTGGCTTCCCCGGATGTTTGGCTACCTCCACCCTCCATCTCAAAGAAATAACATCA	consensus cagcctggcttccccggatgtttggctacctccaccctccatctcaaagaaataacatca	US-10-788- 533	US-10-788- 639	US-10-788- 643		US-10-788- 1587 TCCAITGGGGTAGAAAAGGGGGGGCCGGGGGGGGGGGGGG	
US-10-788- 639	US-10-788- 643	US-10-788- 675	1038	Consensus tgggaaagtccagggactggttaagaaagttggataagattcccccttgcacctcgctgcc HS-10-788- 511		US-10-788- 643	US-10-788- 675	US-10-788- 1099 CATCAGAAAGCCTGGGGGGGGGCCCAGAGCACAACACTGGGGGGCAACTGTAGATGTGGTTTC 	consensus catcagaaagcctgaggcgtgcccagagcacaaagactgggggcaactgtagatgtggtttc	US-10-788- 533	US-10-788- 639	US-10-788- 643	US-10-788- 675	US-10-788- 1160 TAGTCCTGGCTCTGCCACTAACTTGCTGTAACCTTGAACTACAATTCTCCTTCGGGA	US-10-788- 1160 TAGTCCTGGCCTCTGCCACTAACTTGCTGTGTAACCTTGAACTTACAATTCTCCTTTGGGA	consensus tagtcctggctctgccactaacttgctgtgtaaccttgaactacacaattctccttcggga	US-10-788- 533	US-10-788- 639	US-10-788- 643	US-10-788- 675	US-10-788- 1221 CCTCAATTTCCACTTTGTAAAATGAGGGTGGGAGGAGGAATAGGATCTCGAGGAGAGAGA	US-10-788- 1221 CCTCAATTTCCACTTTGTAAAATGAGGGTGGGGAGTGGGAATAGGATCTCGAGGAGATATT	consensus ceteaatttecaetttgtaaaatgagggtggaggggggaataggatetegaggagaetatt	US-10-788- 533	US-10-788- 639 .	US-10-788- 643	US-10-788- 675	1	US-10-788- 1282 GGCATATGATTCCAAGGACTCCAGTGCCTTTTGAATGGGGAGAGGGAGAGAGA	_

consensus tccattggggtagaaaaggagagaggtccgagggtggtgggaggga	US-10-788- 1892 AGAATATTATTGGGGAAAAACTACAAGTGCTGTACATATGCTGAGAAACTGCAGAGCATA
US-10-788- 533	consensus agaatattattgggggaaaaactacaagtgctgtacatatgctgagaaactgcagagcata
US-10-788- 639	US-10-788- 533
US-10-788- 643	US-10-788- 639
US-10-788- 675	US-10-788- 643
US-10-788- 1648 CCCAACTTCCCAAAGAGCAGCATCCCTCCCCGACCCATAGCCATGTTTTAAAGTCACCTT	US-10-788- 675
US-10-788- 1648 CCCAACTTCCCAAAGAGCAGCATCCCTCCCCCGACCCATAGCCATGTTTTAAAGTCACCTT	US-10-788- 1953 ATAGCTGCCACCCAAAATCTTTTTGAAAATCATTTCCAGACAACCTCTTACTTTCTGTGT .
consensus cccaacttcccaaagagcagcatcctcccccgacccatagccatgttttaaagtcacctt	US-10-788- 1953 ATAGCTGCCACCCAAAAATCTTTTGAAAATCATTTCCAGACAACCTCTTACTGTGT
US-10-788- 533	consensus atagctgccaccaaaaatcttttgaaaatcattccagacaacctcttacttctgtgt
US-10-788- 639	US-10-788- 533
US-10-788- 643	US-10-788- 639
US-10-788- 675	US-10-788- 643
US-10-788- 1709 CCGAAGAGAAGTGAAAGGTTCAAGGACACTGGCCTTGCAGGCCCGGAGGGAG	US-10-788- 675
US-10-788- 1709 CCGAAGAGAAGTGAAAGGTTCAAGGACACTGGCCTTGCAGGCCCGAGGGAGCAGCCATCAC	US-10-788- 2014 AGTITITAATIGITAAAAAAAAAAAGTITITAAACAGAGCACACATGACATATGAAAGCCTGC
consensus ccgaagagaagtgaaaggtcaaggacactggccttgcaggcccgagggagacatcac	US-10-788- 2014 AGTITITAATIGITAAAAAAAAAAAGTITITAAACAGAAGCACATGACATATGAAAGCCTGC
US-10-788- 533	consensus agtttttaattgttaaaaaaaaaagttttaaacagaagcacatgacatatgaaagcctgc
US-10-788- 639	US-10-788- 533
US-10-788- 643	US-10-788- 639
US-10-788- 675	US-10-788- 643
US-10-788- 1770 AAACTCACAGACCAGCACATCCTTTTGAGACACCGGCTTCTGCCCACCACGGGACAC	US-10-788- 675
US-10-788- 1770 AAACTCACAGACCAGCACATCCCTTTTGAGACACCGCCTTCTGCCCACTCACT	US-10-788- 2075 AGGACTGGTCGTTTTTTTTGGGAATTCTTCCACGTGGGACTTGTCCACAAGAATGAAAGTAG
consensus aaactcacagaccagcacatcctttgagacaccgccttctgcccaccactcacggacac	US-10-788- 2075 AGGACTIGITITITIGGCAATICITCCACGIGGGACTIGICCACAAGAAGTAG
US-10-788- 533	consengus aggactggtcgtttttttggcaattcttccacgtgggacttgtccacaagaatgaaagtag
US-10-788- 639	US-10-788- 533
US-10-788- 643	US-10-788- 639
US-10-788- 675	US-10-788- 643
US-10-788- 1831 ATTTCTGCCTAGAAAACAGCTTCTTACTGCTCTTACATGTGATGGCATATCTTACACTAAA	US-10-788- 675
US-10-788- 1831 ATTTCTGCCTAGAAACAGCTTCTTACTGCTCTTACATGTGACATATCTTACACTAAA	US-10-788- 2136 IGGITITATAAGAGITAAGITACATATITATITITCICACITAAGITATITATGICAAAAGIT
consensus attictgcctagaaacagcticttactgctcttacatgtgatggcatatcttacactaaa	US-10-788- 2136 TGGTTTTTAAAGGGTTAAGGTTACATATTTATTTTTTTCTCACTTAAGGTTATTATGCAAAAGTT
US-10-788- 533	consensus tggtttttaaagagttaagttacatatttattttctcacttaagttatttat
US-10-788- 639	US-10-788- 533
US-10-788- 643	US-10-788- 639
US-10-788 675	US-10-788- 643
US-10-788- 1892 AGAATATTATTGGGGAAAAACTACAAGTGCTGTACATATGCTGAGAAACTGCAGAGCATA	US-10-788- 675

ATGCTGAGAACTGCAGAGCATA

genalign.rec

tttcttgtagagaatgacaatgttaatattgctttatgaattaacagtctgttcttccaga

US-10-788- 533

consensus

US-10-788- 643

US-10-788- 639

US-10-788- 675

US-10-788- 2258 GTCCAGAGACATTGTTAATAAAGACAATGAATGACGGAAAG US-10-788- 2258 GTCCAGAGACATTGTTAATAAAGACAATGAATCATGACCGAAAG gtccagagacattgttaataaagacaatgaatcatgaccgaaag consensus

Alignment score = -28949.00

Scoring matrix:

2299 -7671 -7754 -7553 -8347 -7673 -7754 -7555 -8348

412 521

396 -106

-249

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June 28, 2005, 14:54:42 ; Search time 10379.5 Seconds (Without alignments) 10741.894 Million cell updates/sec
                                                                                                                                                                     1 agagcctgtgctactggaag..........caatgaatcatgaccgaaag 2301
                                                                                                                                                                                                                                                                           9416466
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                         4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                      GenEmbl: *
                                                                                                                                      Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                .
Database :
                                                                                                                                                                                                                                          Searched:
                                                                                Run on:
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		d			SUMMARIES		
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m	2301	100.0	2301	9	AR267465	AR267465	Sequence
4	2301	100.0	2301	9	AR371665	AR371665	Sequence
S	2301	100.0	2323	σ	AF326739	AF326739	Homo sapi
y	2299.4	99.9	2301	9	BD251907	BD251907	Compositi
7	2299.4	99.9	2301	ø	BD251909	BD251909	Compositi
æ	2299.4	99.9	2301	ø	AR258993	AR258993	Sequence
თ	2299.4	99.9	2301	ø	AR258995	AR258995	Sequence
10	2299.4	6.66	2301	9	AR267466	AR267466	Sequence
11	2299.4	99.9	2301	9	AR267468	AR267468	Seguence
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13	2299.4	99.9	2301	9	AR371668	AR371668	Sequence
14	2297.8	6.66	2301	9	BD251908	BD251908	Compositi
15	2297.8	99.9	2301	ė	AR258994	AR258994	Sequence
16	2297.8	99.9	2301	9	AR267467	AR267467	Sequence
17	2297.8	99.9	2301	9	AR371667	AR371667	Seguence
18	2280.6	99.1	2329	9	AX056687	AX056687	Sequence
19	2280.6	99.1	2329	9	AX574536	AX574536	Sequence
							,

ORIGIN

AY358627 Homo sapi	AP331844 Homo sapi	AX342535 Sequence	AX342537 Sequence	BD251915 Compositi	AR259001 Sequence	AR267474 Sequence	AR371674 Sequence	AF326736 Homo sapi	AC003098 Homo sapi	AC055813 Homo Bapi	AF397423 Homo sapi	AC073954 Homo sapi		AX323453 Sequence	AR259025 Sequence		AR371698 Sequence	BD251910 Compositi	AR258996 Sequence	AR267469 Sequence	AR371669 Sequence	AF326742 Cercopith	BD251912 Compositi		AR267471 Sequence
AY358627	AF331844	AX342535	AX342537	BD251915	AR259001	AR267474	AR371674	AF326736	AC003098	AC055813	AF397423	AC073954	AY358203	AX323453	AR259025	AR267498	AR371698	BD251910	AR258996	AR267469	AR371669	AF326742	BD251912	AR258998	AR267471
σ		_		9		_	9	o	ი	6		7	σ	9	9	ø	_	_	_	ø	_	-	φ	9	9
2329	2296	2271	7099	9301	9301	9301	9301	21501	94752	80117	93790	177744	1154	759	642	642	642	642	642	642	642	642	674	674	674
99.1	98.8	97.7	89.0	89.0	89.0	89.0	89.0	89.0	89.0	88.5	70.1	46.3	36.5	33.0	27.9	27.9	27.9	26.6	26.6	26.6	26.6	26.6	23.3	23.3	23.3
2280.6	2273.2	2248.2	2047.8	2047.8	2047.8	2047.8	2047.8	2047.8	2047.8	2035.8	1612	1066.4	839.6	759	642	642	642	613.2	613.2	613.2	613.2	613.2	536.2	536.2	536.2
20	21	22	23	24	22	56	27	28	53	30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	42
			U						υ	υ		υ													

RESULT 1 BD251906	1
DEFINITION ACCESSION	ĕ
VERSION KEYWORDS	BD251906.1 GI:33061676 . JP 2002531090-A/1.
SOURCE ORGANISM	Homo sapiens (human) Homo sapiens
	Chordata;
REFERENCE	Manusta; buchetta; filmaces; caratinini; nominidae; nomo. 1 (bases 1 to 2301)
AUTHORS	Brunkow, M. E., Galas, D.J., Kovacevich, B., Mulligan, J.T.,
	Paeper, B.W., Ness, J.V. and Winkler, D.G.
TITLE	Compositions and methods for increasing bone mineralization Datent. JD 2002531090-1 1 24-555-2002.
	DARWIN DISCOVERY LTD
COMMENT	
•	
	24-NOV-1999 JP 2
	MARY E BRUNKOW, D
	PI BRYAN W PAEPER, JEFFREY VAN NESS, DAVID G WINKLER PC
	C12N15/09, C12N15/09, A01K67/027, A61K31/713, A61K48/00, A61P19/00, PC
	2
	PC C07K14/47, C07K16/18, C07K19/00, C12N5/10, C12N9/00, C12P21/02, PC
	2821/08,
	PC C12Q1/02, C12Q1/68, G01N33/53, G01N33/53, G01N33/566, C12N15/00, PC
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	CIZNS/00
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FEATURES	Location/Qualifiers
Bource	12301
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 28, 2005, 15:05:42; Search time 8462.86 Seconds (without alignments) 10349.440 Million cell updates/sec Run on:

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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Ligting first 45 summaries

Database :

95 est1: *
95 est2: *
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95 est3: *
95 est6: *
95 est6: *
95 est6: * EST: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOUTHERNIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	1448.2	62.9	1475	m	AF170491	AF170491 Homo sapi
7	1169.6	50.8	1177	m	AF184211	AF184211 Homo sapi
c S	668.4	29.0	685	Ŋ	BU617598	BU617598 UI-H-DF0-
4	658.2	28.6	989	ß	BU621845	BU621845 UI-H-DF0-
ហ	642	27.9	642	o	AY400962	AY400962 Homo sapi
9	550.4	23.9	637	თ	AY400963	AY400963 Pan trogl
7	527.2	22.9	1990	m	AK017295	AK017295 Mus muscu
8	512.4	22.3	540	Н	A1768408	-
σ	506.2	22.0	947	9	BY717106	BY717106 BY717106
10	501.6	21.8	636	0	AY400964	AY400964 Mus muscu
11	494	21.5	494	ß	BX282099	BX282099 BX282099
12	491.2	21.3	667	~	BB636457	BB636457 BB636457
c 13	491	21.3	491	~	AW771508	AW771508 hn57e09.x
14	469.4	20.4	623	7	BB637315	BB637315 BB637315
c 15	457	19.9	468	٦	AI498457	AI498457 tm49e03.x
c 16	452	19.6	466	Н	AI383985	AI383985 te35f02.x
c 17	439.8	19.1	466	Н	AI493134	AI493134 qz50b02.x
c 18	428.4	18.6	452		AA393768	AA393768 zv64f08.8
19	419.4	18.2	432	7	CN258789	CN258789 170005325
c 50	387.4	16.8	414	-	AI498691	AI498691 tm42c02.x
c 21	375.2	16.3	402	Н	AA969408	AA969408 op53b07.8
22	367	15.9	511	~	BB638050	BB638050 BB638050
c 23	351.8	15.3	419	~	BE101082	BE101082 UI-R-BJ1-
c 24	341	14.8	341	Н	AI580267	AI580267 tm45e09.x

	CB425970 601084 MA	AI556282 UI-R-C2p-	AI783624 tz99d03.x	CB418651 591462 MA	CN258788 170005328	AQ171546 HS 3088 B	CR823295 GROAAS3C	AI113131 UI-R-C2p-	BE111224 UI-R-BJI-	CO620016 DG9-202a2	D79813 HUM330C08B	CB432800 609052 MA	CD250782 AGENCOURT	AL922835 AL922835	AA393939 zv64f09.r	BF523030 UI-R-C2p-	BB221258 BB221258	BJ712074 BJ712074	CB762755 AMGNNUC:T	BB212560 BB212560
BF431247	CB425970	AI556282	AI783624	CB418651	CN258788	AQ171546	CR823295	AI113131	BE111224	C0620016	D79813	CB432800	CD250782	AL922835	AA393939	BF523030	BB221258	BJ712074	CB762755	RR212560
N	9	-	н	9	7	æ	σ	н	7	7	7	9	9	н	-	~	~	4	9	ç
352	498	360	329	704	269	535	732	315	291	548	271	648	221	532	180	254	643	716	423	476
14.6	14.0	13.3	12.8	12.1	11.5	11.3	11.2	11.1	10.6	10.1	10.0	9.5	8.3	7.1	7.0	6.9	6.7	6.7	9.9	u u
332	321.8	306.2	294	278.2	264.2	260.6	256.6	255.8	243	233	229.4	219.2	190.4	163.2	161.2	158.8	153.8	153.8	151.6	150
		7	8	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
25	56	N	. 4	• •																

ALIGNMENTS

RESULT 1	
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rocas	AF170491 1475 bp mRNA linear HTC 01-AUG-2003
DEFINITION	Homo sapiens MSTP078 (MST078) mRNA, complete cds.
ACCESSION	AF170491
VERSION	AF170491.1 GI:33337957
KEYWORDS	HTC.
SOURCE	Homo sapiens (human)
ORGANISM	Нощо варіепв
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Primates;
REFERENCE	1 (bases 1 to 1475)
AUTHORS	Hui, R.T., Qin, B.M., Sheng, H., Liu, Y.Q., Zhao, B., Liu, B., Wang, X.Y.,
	Zhang, Q., Song, L., Gao, Y., Zhang, C.L., Ye, J., Ji, X.J., Liu, B.H.,
	Lu, H., Xu, H.S., Chen, J.Z., Cai, M.O., Zheng, W.Y., Teng, C.Y., Liu, Q.,
	Yu, L.T., Lin, J., Gong, Q., Zhang, A.M. and Gao, R.L.
TITLE	Homo sapiens normal aorta mRNA MST078
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1475)
AUTHORS	Hui, R.T., Oin, B.M., Shenq, H., Liu, Y.Q., Zhao, B., Liu, B., Wang, X.Y.,
	Zhang, O., Song, L., Gao, X., Zhang, C.L., Ye, J., Ji, X.J., Liu, B.H.,
	Lu, H., Xu, H.S., Chen, J.Z., Cai, M.Q., Zheng, W.Y., Teng, C.Y., Liu, Q.,
	Yu. L. T., Lin, J., Gong, O., Zhang, A.M. and Gao, R.L.
TITLE	Direct Submission
JOURNAL	Submitted (19-JUL-1999) Molecular Medicine Center for
	ute.
PEATTRES	Location/Malifiers
au lius	1 1 1 7 7 5
	/ordentem="Homo ganteng"
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attab	1. 14.0
ć	Control (1)
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Query Match

ORIGIN

62.9%; Score 1448.2; DB 3; Length 1475;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

June 28, 2005, 14:54:42 ; Search time 1340.09 Seconds (without alignments) 10164.517 Million cell updates/sec Run on:

US-10-788-606-1

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Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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genesequ2003bs:*
genesequ2003ds:*
genesequ2004as:*
genesequ2004bs:* N Geneseq 16Dec04:* geneseqn2002as:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs: geneseqn2002bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaa29055 Human TGF	Ads12958 TGF-beta	Acf79824 Human SOS	Aaa29061 Mutant hu	Aaa29062 Human TGF	Ads12964 TGF-beta	Ads12960 TGF-beta	Aaa29056 Human TGF	Ads12962 TGF-beta	Aaa91023 Human sec	Abk69992 cDNA enco	Ada01331 Human PRO	Ada43760 Human cDN	Ada43528 Human cDN	Ada01203 Human PRO	Ada01087 Human cDN	Ada43644 Human cDN	Ada06906 Human PRO	Novel	Adb99687 Human PRO
•	a	AAA29055	ADS12958	ACF79824	AAA29061	AAA29062	ADS12964	ADS12960	AAA29056	ADS12962	AAA91023	ABK69992	ADA01331	ADA43760	ADA43528	ADA01203	ADA01087	ADA43644	ADA06906	ADA08394	ADB99687
	BB	<u>س</u>	13	10	m	m	13	13	m	13	ず	ø	σ	6	δ	σ	σ	σ	σ	σ	σ
	Query Match Length DB	2301	2301	2323	2301	2301	2301	2301	2301	2301	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329
من	Query Match	100.0	100.0	100.0	99.9	99.9	99.9	99.9	99.9	99.9	1.66	99.1	99.1	99.1	1.66	99.1	99.1	99.1	99.1	99.1	99.1
	Score	2301	2301	2301	2299.4	2299.4	2299.4	2299.4	2297.8	2297.8	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6
	Regult No.		7	٣	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20

Claim 1; Page 114-115; 162pp; English.

Human	Human c	Adb99803 Human PRO	Adb99458 Novel hum	Adb66009 Human cDN	Human	O Human	7 Human	Human	Human	Human	Human	Ade38164 Human PRO	Human C	Add90861 Human cDN	Juman	Adg06509 Human PRO	fuman	Juman	Tuman	Ade51830 Human cDN	Ade37688 Human cDN	Ade37572 Human cDN	Add95343 Human cDN	Ade38043 Human PRO
ADB86970	ADB66125	ADB99803	ADB99458	ADB66009	ADC23407	ADC26100	ADE04927	ADB11233	ADD88164	ADD95459	ADE06389	ADE38164	ADD88280	ADD90861	ADF99416	ADG06509	ADG05460	ADG82461	ADE51714	ADE51830	ADE37688	ADE37572	ADD95343	ADE38043
σ	σ	2	ដ	10	10	2	10	10	10	10	10	20	70	10	10	10	10	ដ	12	12	12	12	12	12
2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329	2329
. 99.1	99.1	1.66	99.1	99.1	1.66	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	1.66	99.1	99.1	99.1	1.66	99.1	99.1	99.1	1.66
2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6	2280.6
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; chromosome 17q12-21; gene therapy; antisense therapy; fracture; bone mineralization; ss.
                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures.
                                                                                                                                                                                                                                                                                                               Paeper BW;
                                                                                                                                                          Location/Qualifiers
48. .689
/*tag= a
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                                                                                                                                                                                                                                                     99WO-US027990.
                                                                                                                                                                                                                                                                         98US-0110283P.
                                                                                                                                                                                                                                                                                            (DARW-) DARWIN DISCOVERY LTD.
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                 Galas DJ, 1
Winkler DG;
                                                                                                                                                                                                                                                                                                                                             WPI; 2000-412321/35.
P-PSDB; AAY96429.
                                                                                                                                                                                                               WO200032773-A1
                                                                                                                                                                                                                                                      24-NOV-1999;
                                                                                                                                                                                                                                                                         27-NOV-1998;
                                                                                                                                          Homo sapiens
                                                          12-SEP-2000
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June 28, 2005, 15:15:06; Search time 1539.09 Seconds (without alignments) 9344.794 Million.cell updates/sec
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pubpna/US10I_PUBCOMB.eed
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                       6067389 seqs, 3125258755 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:
                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 08
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Sequence 1, Appli
Sequence 1, Appli
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   Result
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W. T. W. T.	, , , , , , , , , , , , , , , , , , ,			educince os,
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APPLICANT: Paepers. Bryan W.
APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING TITLE OF INVENTION: BONE MINERALIZATION
FILE REFERENCE: 240083.508D5
CURRENT APPLICATION NUMBER: US/10/384,893
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PARESEQ for Windows Version 3.0
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Sequence 1, Application US/10384893
Publication No. US20030166247A1
                                                                             APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
; ORGANISM: Homo sapien
US-10-384-893-1
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LENGTH: 2301
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| Cgm2 6/ptodata/1/pma/USO8 COMB. seq:*
| Cgm2 6/ptodata/1/pma/USO9 COMB. seq:*
| Cgm2 6/ptodat
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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June 28, 2005, 14:55:24; Search time 1618.95 Seconds (without alignments) 6348.430 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES

Sequence 13845, A	Sequence 12371, A	Sequence 16122, A	Sequence 97309, A	Sequence 2, Appli	Sequence 1016, Ap	5332	Seguence 1684, Ap	Seguence 7216, Ap	Sequence 35, Appl	Sequence 26, Appl	Sequence 1355, Ap	Sequence 689, App	Sequence 1989, Ap		3092	Sequence 433, App	Sequence 73, Appl	Sequence 1197, Ap		Sequence 4826, Ap		1476,	1198,	1199,	Sequence 2, Appli	Sequence 2, Appli	
US-10-940-774A-13845	US-10-940-774A-12371	US-10-940-774A-16122	US-10-990-328A-97309	US-11-121-086-2	US-11-031-175-1016	US-10-703-032-15332	US-10-703-032-1684	US-60-669-175-7216	US-10-939-036-35	US-60-662-220-26	PCT-IB03-06509-1355	US-10-489-448-689	US-11-090-997-1989	US-11-021-825-1	US-10-940-774A-3092	US-11-000-688A-433	US-11-080-991-73	US-11-085-606-1197	. US-11-154-939-4825	11-154-939-	US-60-651-509-1475	US-60-651-509-1476	US-11-085-606-1198	US-11-085-606-1199	US-11-101-000-2	US-11-130-945-2	
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51	21	50.6	50.6	50.6	50.4	50.2	50.2	20	49.6	49.4	49.4	49.2	49.2	49.2	49	49	49	49	49	49	.49	49	49	49	49	49	
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-668-037A-7

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US-09-668-031A-7

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13,	Sequence 13, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl	Sequence 11, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl	17,11	Sequence 9816, Ap Sequence 40, Appl
US-09-449-218D-13 US-09-668-529A-13 US-09-668-037A-13	US-09-668-021-13 US-09-449-218D-11 US-09-668-529A-11 US-09-668-037A-11	US-09-668-021-11 US-09-449-218D-15 US-09-668-529A-15	US-09-668-021-15 US-09-449-218D-17 US-09-668-529A-17 US-09-668-037A-17 US-09-668-021-17	US-09-513-999C-9816 US-09-188-930-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                            GENERAL INFORMATION:
APPLICANT: Balas, David J.
APPLICANT: Galas, David J.
APPLICANT: Galas, David J.
APPLICANT: Wulligan, John T.
APPLICANT: Paper: Bryan W.
APPLICANT: Paper: David G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING TITLE OF INVENTION: BOND MINERALIZATION
TITLE OF INVENTION: 1999-11-24
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2301; Conservative 0; Mismatches
Sequence 1, Application US/09449218D Patent No. 6395511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
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June 28, 2005, 14:54:42; Search time 10379.5 Seconds (without alignments) 10741.894 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                  4708233 seqs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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	рв	9	9	v	9	ø	ø	ø	9	9	ø	9	ø	σ	ø	ø	9	9	ø	ý
	Query Match Length	2301	2301	2301	2301	2301	2301	2301	2301	2301	2301	2301	2301	2323	2301	2301	2301	2301	2329	2329
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σ	σ	ø	9	9	φ	9	9	6	σ	o	σ	~	σ	9	ø	φ	ø	9	9	v	9	σ	ø	φ	9
2329	2296	2271	7099	9301	9301	9301	.9301	21501	94752	80117	93790	177744	1154	759	642	642	642	642	642	642	642	642	674	674	674
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June 28, 2005, 15:05:42 ; Search time 8462.86 Seconds (without alignments) 10349.440 Million cell updates/sec
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Perfect score:
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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	цo	Homo sapi	Homo sapi	UI-H-DF0	UI-H-DF0	Homo sapi	Pan trog	Mus muscu	wh14c03.x	BY717106	Mus muscu	BB636457	hn57e09.x	BX282099	BB637315	tm49e03.x	te35f02.x	qz50b02.x	zv64f08.8	170005325	tm42c02.x	op53b07.8	BB638050	UI-R-BJ1-	tm45e09.x
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IES																									
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	DB	м	m	ß	Ŋ	σ	o	m	Н	y	σ	~	~	ß	~	ч	Н	Н	Н	7	Н	,	~	~	Н
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	& Query Match	62.9	50.8	29.0	28.6	27.8	23.8	22.9	22.3	22.0	21.8	21.3	21.3	21.3	20.4	19.9	19.6	19.1	18.6	18.2	16.8	16.3	15.9	15.3	14.8
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	124																								

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	DEFINITION	iens MSTP078 (MST078) mRNA,
	ACCESSION	AF170491
	VERSION	AF170491.1 GI:33337957
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		Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
	REFERENCE	1 (bases 1 to 1475)
	AUTHORS	Hui, R.T., Qin, B.M., Sheng, H., Liu, Y.Q., Zhao, B., Liu, B., Wang, X.Y.,
		Zhang, Q., Song, L., Gao, Y., Zhang, C.L., Ye, J., Ji, X.J., Liu, B.H.,
	٠	Lu, H., Xu, H.S., Chen, O. Z., Cal, M.Q., Zheng, W.T., Teng, C.T., Liu, Q.,
	i	ru, L. T., Lin, U., Gong, L., Zhang, A. M. and Gao, K. L.
	TITLE	HOMO BADJERS NOTHAL AOILA MKNA MSIU/8
	REFERENCE	Onpublished 2 (bases 1 to 1475)
	AUTHORS	Hui.R.T. oin.B.M. Sheng.H. Liu.Y.O., Zhao.B., Liu.B., Wang, X.Y.,
		Shang O Song I. Gao V Shang C I. Ve J. Ji K J. Liu B H.
		Lu. H., Xu.H.S., Chen.J.Z., Cai.M.O., Zheng.W.Y., Teng.C.Y., Liu.O.,
		Yu. L. T. Lin. J., Gong, O., Zhang, A.M. and Gao, R.L.
	TITLE	Direct Submission
	JOURNAL	Submitted (19-JUL-1999) Molecular Medicine Center for
		Cardiovascular Disease, Cardiovascular Institute, CAMS and PUMC,
		167, Bei Li Shi Lu, Beijing 100037, P.R.China
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	ORIGIN	vacaco.
	N	ob 62 0\$. Same 1448 3. Length 1475.
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June 28, 2005, 14:54:42; Search time 1340.09 Seconds (without alignments) 10164.517 Million cell updates/sec
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genesequ2000s:*
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2301
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AAA29056 standard; cDNA; 2301 BP.

AAA29056

AAA29056;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ada12960 TGF-beta Aaa91023 Human 8ec Abk69992 CDNA enco Ada43760 Human CDN Ada43528 Human CDN Ada43528 Human CDN Ada61203 Human CDN Ada66906 Human CDN Ada66906 Human RRO Ada699687 Human PRO Ads12958 TGF-beta Acf79824 Human SOS Aaa29061 Mutant hu Ada29062 Human TGF Ads12964 TGF-beta Aaa29055 Human TGF Aaa29056 Human TGF Description SUMMARIES ADA43760 ADA01331 Query Match Length DB 2301 2277.4 2301 Score 2296.2 2297.8 2297.8 2299.4 2296.2 Result Š.

Adb86970 Human PRO	Human c		Novel	Human	Adc23407 Human cDN	Human	7 Human	Human	4 Human	Human	Human	Human	Human	1 Human	Human		Human	Human	Ade51714 Human cDN	Ade51830 Human cDN	Human	2 Human	Add95343 Human cDN	Ade38043 Human PRO		
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2329 9	2329 9		2329 1	-	1		1	-				2329 1	··				О	σ.	σ.		О	σ.	σ.	6		
99.0		99	99.	99	66	99	99	66	66	99	99.	99.	99.	99.	99.	99.0	99.	99.		99		99		99.		
2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	277	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	2277.4	7		
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5		•

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osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; variant; V101; gene therapy; antisense therapy; fracture; chromosome 17q12-21; bone mineralization; 88.
                                                                                                                                                                                                                                                                                                                                                   Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures.
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                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                               98US-0110283P
                                                                                                                                                                                                                                                                    (DARW-) DARWIN DISCOVERY LTD
          12-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                        Galas DJ,
Winkler DG;
                                                                                                                                                                                                                                                                                                                        WPI; 2000-412321/35.
P-PSDB; AAY96430.
                                                                                                                                                                                 WO200032773-A1
                                                                                                                                                                                                                                                27-NOV-1998;
                                                                                                                                                                                                                           24-NOV-1999;
                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                         Brunkow ME,
Van Ness J,
                                                                                                                                                                                                      08-JUN-2000
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Claim 1; Page 118-119; 162pp; English.

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June 28, 2005, 15:15:06; Search time 1539.09 Seconds (without alignments) 9344.794 Million cell updates/sec
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1: \( \cgn2 \) \( \cgn \) 
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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0; Gaps

1 AGAGCCTGTGCTACTGGAAGGTGGCGTGCCCTCCTCGGCTGGTACCATGCAGCTCCCAC 60

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Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2301; Conservative 0; Mismatches 0; Indels 0;

equence 7,		Seguence 7,	Sequence 61,	Sequence 1, Sequence 1,	Sequence 1,	Sequence 1,	Sequence 57,	Sequence 2,	Sequence 3,	Sequence 3,	Sequence 3, Appli Sequence 3, Appli	Sequence 63	Sequence 63	Sequence 63	Sequence 63	Sequence 63	Sequence 63	Sequence 63	Sequence 63	Sequence 63	Sequence 63,	Sequence 63,	Sequence	Sequence 63,	Sequence 63,	Sequence 63.	3 Sequence										FOR INCREASING					€.		
7 US-10-463-190-	8 US-10-0	1 US-1(1 US-1(0 0S-10 7 US-10	8 US-1(9 US-1(1 US-10-868-497-5	7 US-1(0S-10-384-893-37 US-10-463-190-3	8 US-10-095-248A-	9 US-10-788-606-3 1 US-10-799-162-3	4 US-10-245-752-6	4 US-10-245-859-6	4 US-10-245-103-6 4 US-10-245-107-6	4 US-10-245-143-6	4 US-10-245-771-6	4 US-10-245-831-6 4 US-10-245-883-6	4 US-10-237-535-6	4 US-10-238-183-6	4 US-10-238-283-6 4 US-10-238-370-6	4 US-10-245-055-6	4 US-10-245-147-6	.245-739-6	246-210-6	239-196-6	10-243-024-6	10-245-621-6	ALIGNMENTS		384893	14		•			λ.,	HODS	INERALIZATION	US/10/384,893	3-06	ws Version 3.0			
9.9 2301	9.9 2301	9.9 2301	99.9 2301	99.9 2301	99.9 2301	99.9 2301	99.9 2301	99.9 2323	99.8 2301 99.8 2301	99.8 2301	99.8 2301 1	99.0 2329	99.0 2329	99.0 2329 99.0 2329	99.0 2329	9.0 2329	2323 0.6	9.0 2329	9.0 2329	9.0 2329	9.0	9.0 2329	9.0	9.0	9.0	0.0	9.0		، س	Application US/103848	INFORMATION:	Brunkow, Mary E.	Galas, David J.	Mulligan, John 7	T: Paeper, Bryan W.	Van Ness, Jeffre	VENTION: COMPOSIT	WENTION: BONE M	PERENCE: 240083.508D5 APPLICATION NUMBER: US/10/384.89	ING DATE: 2003-		2301 4	Homo sapien)
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Database

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6348.430 Million cell updates/sec
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Seguence 16122, A	Sequence 97309, A		Sequence 1016, Ap	5332	Seguence 1684, Ap	Sequence 7216, Ap	Sequence 35, Appl	Sequence 26, Appl	Seguence 13845, A	Sequence 12371, A	Sequence 1355, Ap	Sequence 689, App	Sequence 1989, Ap	Sequence 1, Appli	Sequence 3092, Ap		73,	119	Sequence 4825, Ap	4	Sequence 1475, Ap		Sequence 1198, Ap	113	'n	Sequence 2, Appli
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APPLICANT: Szak, Suzanne
APPLICANT: 1, Huo
APPLICANT: Li, Huo
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE OF INVENTION: Pragments of, Cynomolgus Monkey Genes and the Use Thereof
TITLE REPERENCE: 2159029000
CURRENT APPLICATION NUMBER: US/60/680,544
CURRENT PILING DATE: 2005-05-13
NUMBER: OF SEQ ID NOS: 48714
SOFTWARE: Patent Sequence Analysis Tool Version 1.0
SEQ ID NO 44583
LENGTH: 2302
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                   Sequence 44583, Application US/60680544 GENERAL INFORMATION:
                                                                        APPLICANT: Cooper, Matthew
APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramaniam, S. Sai
APPLICANT: Szak, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-60-680-544-44583
US-60-680-544-44583
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June 28, 2005, 15:03:06; Search time 404.818 Seconds (without alignments) 9300.665 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1 agagcotgtgctactggaag..........caatgaatcatgaccgaaag 2301 2405568 Total number of hits satisfying chosen parameters: 1202784 segs, 818138359 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-10-788-606-5 2301 Scoring table: Title: Perfect score: Sequence: Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appli Sequence 5, Sequence 45 Sequence 9, Sequence 5, Sequence 5, Sequence 5, Sequence 7, Sequence 7 Sequence 1 Sequence 1 Description Sequence 3 Sequence 3 Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence -09-668-021-3 -09-449-218D-18 8-037A-18 .09-449-218D-45 8 Query Match Length 23301 23301 23301 23301 23301 23301 23301 23301 23301 23301 23301 2299.4 2299.4 2297.8 Score Result Š.

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AR258025 Sequence
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Sequence Sequence Homo sapi Sequence

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1 (bases 1 to 642)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wanno, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, W. Homen, M.D. and Cargill, D. Endering nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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June 28, 2005, 14:54:42, ; Search time 373.896 Seconds (without alignments) 10164.517 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Description	Ada27200 Monkey LR Ads12720 Monkey LR Ads12720 Monkey LR Ads24051 Human DAN Ads27109 Human Clo Add27576 Human Ost Ads127576 Human Ost Ads1259 TGF-beta AGF1924 Human Ost Ads1296 TGF-beta AGF1925 Human Ost Ads1296 Human Ost Ads1298 Human Oby Ads1311 Human PRO Ads1311 Human CDN Ads1351 Human CDN Ads1352 Human CDN Ads1354 Human CDN
SUMMARIES	AAA29057 AD127200 AAA29051 AAA94051 AAA94203 ABA94239 AAA29055 AAA29055 AAA312958 AAA312958 AAA31023 AAA31023 AAA31023 AAA31023 AAA31023 AAA31023 AAA31023 AAA31023 AAA310331 AAA310333
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June 28, 2005, 15:15:06; Search time 429.419 Seconds (without alignments) 9344.794 Million cell updates/sec
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2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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			Description	Sequence 9, Appli	Sequence 9, Appli	Sequence 101, App	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 63, Appl
SOMMAKIBS			ΩI	16 US-10-384-893-9	US-10-463-190-9	US-10-464-368-101	US-10-095-248A-9	US-10-788-606-9	US-10-799-162-9	US-10-868-497-63
			DB	16	1.7	11	18	13	21	21
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Length 642;

Query Match
100.0%; Score 642; DB 16; Length 64
Best Local Similarity 100.0%; Pred. No. 7.1e-166;
Matches 642; Conservative 0; Mismatches 0; Indels

; TYPE: DNA.; ORGANISM: Cercopithecus pygerythrus US-10-384-893-9

1 ATGCAGCTCCCACTGGCCCTGTGTCTTGTCTGCTGCTGGTACACGCAGCCTTCCGTGTA 60

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Appl	Appl	Appl	pli	ppli	ppli	pp.1	ppli	ildd,	Appl	pp11	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appr	Appl	Appl	יות לי היית לי	Appl	ולקלי מעלי	Appl	App1	3, Appl																			
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ptodata/1/pna/US093B_COMB.seq:*/
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ptodata/1/pna/US095D_COMB.seq:*
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6/ptodata/1/pna/USO83_COMB.seq:*
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Maximum Match 100%
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45: /cgn2_6/prodata1//pna/US0956_COMB.Seq; 46: /cgn2_6/prodata1//pna/US0956_COMB.Seq; 46: /cgn2_6/prodata1//pna/US0956_COMB.Seq; 46: /cgn2_6/prodata1/pna/US010B_COMB.Seq; 46: /cgn2_6/prodata1/pna/US
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2005, 14:55:24; Search time 451.701 Seconds (without alignments)

Fitle: (Without alignments)

Forfect score: 642

Sequence: 1 atgcagctcccactggccct.....agctggagaacgcctactag 642

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 13027057 seqs, 2233325459 residues

Total number of hits satisfying chosen parameters: 26054114

Minimum DB seq length: 0

Maximum Match 0*

Maximum Match 0*

Maximum Match 100*

Listing first 45 summaries
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SUMMARIES

Result		* Ouery					
No.	Score	Match	Match Length DB	DB	QI	Description	
	613.2	95.5	2302	15	US-60-680-544-44583	Sequence 44583,	44583,
1 7	613.2	95.5	2302	15	US-60-680-473-44583	Sequence	44583, 1
m	544.4	84.8	570	15	US-60-677-583-99	Sequence	
	75.2	11.7	1089	15	US-60-680-544-23752	Seguence	23752,
· LCT	75.2	11.7	1089	15	US-60-680-473-23752	Sequence 23752,	23752,
9	71	11.1	2337	н	PCT-US05-13260-1	Sequence 1;	, Appli
7	54.2	8.4	152132	11	US-10-940-774A-13845	Seguence 13845,	13845,
- α	54.2	8.4	152145	11	US-10-940-774A-12371	Sequence 12371	12371,
0	52.4	8.5	1917	Φ	US-10-703-032-28735	Sequence 28735, A	8735, A
10	49.6	7.7	1149	7	US-10-990-000-13	Sequence 13,	3, Appl
11	49.6	7.7	28493	13	US-11-031-175-1241	Seguence	1241, A
0 12	49.4	7.7	2323	11	US-10-990-328A-2709	Sequence 2709	2709, A
c 13	49.4	7.7	2382	11	US-10-990-328A-2704	Sequence	2704, A
c 14	49.4	7.7	2440	11	US-10-990-328A-2707	Sequence	2707, A
c 15	49.4	7.7	2642	1	US-10-990-328A-2705	Seguence	2705, A
c 16	49.4	7.7	2701	=======================================	US-10-990-328A-2706	Sequence	2706, A
17	49.4	7.7	25703	11	US-10-990-328A-97405	Sequence	97405,
c 18	49.4	7.7	52112	11	US-10-990-328A-94429	Sequence	94429,

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Sequence 7216, Ap	Sequence 977, App	Sequence 4897, Ap	Sequence 13, Appl	Sequence 3030, Ap	Sequence 875, App	Sequence 1715, Ap	Sequence 1176, Ap	Seguence 2048, Ap	Sequence 12182, A	Seguence 1355, Ap	Sequence 48429, A	48429,	Sequence 4511, Ap	Sequence 9087, Ap		Sequence 1072, Ap	Sequence 96899, A	Sequence 53824, A	Sequence. 11856, A	Seguence 97071, A	Sequence 96632, A	Sequence 31002, A	Sequence 74411, A	Seguence 3, Appli	Sequence 1355, Ap	Segmence 52, Appl	
US-60-669-175-7216	US-11-031-175-977	US-11-031-175-4897	US-10-517-441-13	US-11-154-939-3030	US-60-651-509-875	US-60-664-936-1715	US-60-679-970-1176	US-60-680-002-2048	US-60-659-397-12182	PCT-IB03-06509-1355	US-60-680-544-48429	US-60-680-473-48429	US-11-031-175-4511	US-11-031-175-9087	US-11-031-175-1031	US-11-031-175-1072	US-10-990-328A-96899	US-10-703-032-53824	US-10-703-032-11856	US-10-703-032-97071	US-10-703-032-96632	US-10-703-032-31002	US-10-703-032-74411	US-11-147-109-3	PCT-IB03-06509-1355	112-11-100-356-52	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo Sapiens
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US-09-668-031A-3
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APPLICANT: Brunkow, Mary E.
APPLICANT: Abales, David J.
APPLICANT: Avacevich, Brian
APPLICANT: Mulligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Winkler, Bryan W.
TAPLICANT: Winkler, David G.
TITLE OF INVENTION: BOND MINERALIZATION
FILE REFERENCE: 240083.508
CURRENT APPLICATION NUMBER: US/09/449,218D
CURRENT FILING DATE: 1939-11-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PARLESQ for Windows Version 3.0
SEQ ID NO 9
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US-09-449-218D-9
Sequence 9, Application US/09449218D Patent No. 6395511
GENERAL INFORMATION:
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SOURCE
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/organism='Mus musculus (mouse)'. Location/Qualifiers

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK017295 1990 bp mRNA linear HTC 03-APR-2004 Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430411E23 product:sclerostin, full insert sequence.
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Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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Punctional annotation of a full-length mouse CDNA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC, CAP trapper.
Mus musculus (house mouse)
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us-10-788-606-11.rng

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

June 28, 2005, 14:54:42 ; Search time 371.567 Seconds (without alignments) 10164.517 Million cell updates/sec Run on:

US-10-788-606-11 638

1 atgcagccctcactagcccc......ctggagaacgcctactagag 638 score: Sequence: Title: Perfect

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4390206 segs, 2959870667 residues

Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaa29058 Murine TG	Ads12968 TGF-beta	Adi27106 Mouse LRP	Aba94294 Mouse clo	Acf79826 Mouse SOS	Adi27108 Mouse LRP	Aaa29059 Rat TGF-b	Acf79827 Rat SOST	Adi27113 Rat LRP b	Ads12970 TGF-beta	Aaa29057 Vervet TG	Adi27200 Monkey LR	Ads12966 TGF-beta	Aba94293 Human clo	. Aad27576 Human ost	Aaa29056 Human TGF	Aaa29055 Human TGF	Ads12958 TGF-beta	Ads12962 TGF-beta	Acf79824 Human SOS
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ALIGNMENTS

osteopathic, transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization; ss. Murine TGF-beta binding protein (BEER) cDNA. AAA29058 standard; cDNA; 638 BP. (first entry) Mus musculus. 12-SEP-2000 AAA29058; AAA29058 ID AAA2 XX RESULT 1

Location/Qualifiers
1. .636
/*tag= a
/product= "TGF-beta_binding_protein" Key

WO200032773-A1

08-JUN-2000.

99WO-US027990 24-NOV-1999;

98US-0110283P. 27-NOV-1998; (DARW-) DARWIN DISCOVERY LTD.

Paeper BW; Mulligan JT, Kovacevich B, Galas DJ, Winkler DG; Brunkow ME, Van Ness J,

WPI; 2000-412321/35. P-PSDB; AAY96432.

Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures.

Claim 1; Page 123; 162pp; English.

This cDNA encodes a murine transforming growth factor-beta (TGR-beta)

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9417.841 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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COMB. seg:

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                                                                                                      June 28, 2005, 14:55:24; Search time 448.886 Seconds (without alignments) 6348.430 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-60-680-473-46033

US-60-680-473-46033

US-10-080-1355

US-10-175-175-1731

US-11-097-143-20867

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APPLICANT: Subramaniam, S. sal
APPLICANT: Stak, Suzanne
APPLICANT: Szak, Suzanne
APPLICANT: Szak, Suzanne
APPLICANT: Szak, Suzanne
APPLICANT: Li, Huo
APPLICANT: Bandaru, Raj
APPLICANT: Bandaru, Raj
APPLICANT: Bendaru, Raj
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Presements of, Cynomolgus Monkey Genes and the Use Thereof
FILE REFERENCE: 21590290000
CURRENT APPLICATION NUMBER: US/60/680,544
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 48714
SOFTHARE: Patent Sequence Analysis Tool Version 1.0
SEQ ID NO 44583
LENGTH: 2302
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Sequence 57, Appl
Sequence 57, Appl
Sequence 56, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 12, Appl
Sequence 54, Appl
Sequence 64, Appl
Sequence 6431, Appl
Sequence 6431, Appl
Sequence 6431, Appl
Sequence 66, Appl
Sequence 66, Appl
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Sequence 7810, Ap
Sequence 20822, A
Sequence 20821, A
Sequence 778, App
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Sequence 1355, Ap
Sequence 469, App
Sequence 1193, Ap
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Sequence 28735, A
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13 US-11-031-175-1241
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14 US-10-703-032-28735
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APPLICANT: Kinch, Deborah
APPLICANT: Rosenberg, Michael
APPLICANT: Subramanlam, S. Sai
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Sequence 11, Application US/09449218D

GENERAL INFORMATION:

APPLICANT: Brunkow, Mary E.

APPLICANT: Kovacevich, Brian

APPLICANT: Kovacevich, Brian

APPLICANT: Walligan, John T.

APPLICANT: Walligan, John T.

APPLICANT: Walligan, John T.

APPLICANT: Walling, David G.

TITLE OF INVENTION: BONE MINERALIZATION

TITLE OF INVENTION: BONE MINERALIZATION

TITLE OF INVENTION: BONE MINERALIZATION

TITLE OF INVENTION: UNWERE: 1999-11-24

CURRENT APPLICATION NUMBER: 1999-11-24

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 11

FENCH: 38
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CORGANISM: Mus musculus
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GenCore version 5.1.6 Copyright (c) 1993 - 2005. Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: June 28, 2005, 14:54:42; Search time 3040.32 Seconds (without alignments) 10741.894 Million cell updates/sec Title: US-10-788-606-13 Perfect score: 674 Sequence: 1 qaqqacqqqtqcccttcctaqctqqaqaaqqcctactaq 674	able: IDENTITY_NUC Gapop 10.0, Gapext 1.0 4708233 seqs, 24227607955 residues ber of hits satisfying chosen parameters: 9416466 B seq length: 0 B seq length: 2000000000 B seq length: 2 whimum Match 0 % Maximum Match 100 % Listing first 45 summaries	Database : GenEmbl:* 1: gb ba:* 2: gb_htg:* 3: gb_ni* 4: gb_om:* 5: gb_pi:* 6: gb_pi:* 10: gb_ro:* 11: gb_ro:* 12: gb_sy:* 13: gb_un:* 14: gb_vi:*	er of results predicted by chance to have equal to the score of the result being lysis of the total score distribution. SUMMARIES DB ID Descript	1 674 100.0 674 6 AB251912 BD255912 Compositi 2 674 100.0 674 6 AR267471 AR25899 AR25899 SQUence 4 674 100.0 674 6 AR371671 AR371671 Sequence 5 674 100.0 674 6 AR371671 AR371671 AR371671 Sequence 6 557.6 82.5 63 6 AX323455 AX32455 Sequence 7 556 82.5 638 6 AR267470 AR322455 Sequence 9 556 82.5 638 6 AR267470 AR371670 Sequence 10 556 82.5 638 6 AR371670 AR267470 AR267470 AR267470 Sequence 11 556 82.5 638 6 AR371670 AR267481 AR326740 AR3327670 AR3327670 <td< td=""></td<>

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 28, 2005, 14:54:42; Search time 392.533 Seconds (without alignments) 10164.517 Million cell updates/sec Run on:

US-10-788-606-13 Title:

Perfect score:

1 gaggaccgagtgcccttcct.....agctggagaacgcctactag 674 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaa29059 Rat TGF-b	Acf79827 Rat SOST	Adi27113 Rat LRP b	Ads12970 TGF-beta	Aba94294 Mouse clo	Acf79826 Mouse SOS	Adi27106 Mouse LRP	Aaa29058 Murine TG	Ads12968 TGF-beta	Aba94293 Human clo	Aaa29055 Human TGF	Ads12958 TGF-beta	Acf79824 Human SOS	Aaa91023 Human sec	Abk69992 cDNA enco	Ada01331 Human PRO	Ada43760 Human cDN	Ada43528 Human cDN	Ada01203 Human PRO	Ada01087 Human cDN
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22	23	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Rat TGF-beta binding protein (BEER) cDNA. AAA29059 standard; cDNA; 674 BP. (first entry) 12-SEP-2000 AAA29059; AAA29059

osteopathic, transforming growth factor-beta; TGF-beta; binding protein; BEER, gene therapy, antisense therapy; fracture; bone mineralization; ss.

Rattus norvegicus.

Location/Qualifiers 33. .674 /*tag= a /product= "TGF-beta_binding_protein" WO200032773-A1. Key

99WO-US027990. 98US-0110283P. 24-NOV-1999; 27-NOV-1998;

08-JUN-2000.

(DARW-) DARWIN DISCOVERY LTD.

Paeper BW; Kovacevich B, Mulligan JT, Galas DJ, | Winkler DG; Brunkow ME, Van Ness J,

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WPI; 2000-412321/35. P-PSDB; AAY96433.

Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures.

Claim 1; Page 125; 162pp; English.

This cDNA encodes a rat transforming growth factor-beta (TGF-beta)

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Sequence 1, Appli

Sequence Sequence 3

Sequence

1, Appli 1, Appli 1, Appli 1, Appli 1, Appli 1, Appli 2, Appli 63, Appl 63, Appl

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; ORGANISM: Rattus norvegicus
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SUMMARIES

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4	68	10.1	1089	15	US-60-680-544-23752	Sequence 23752, A
ľ	68	10.1	1089	15	US-60-680-473-23752	Sequence 23752, A
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σ	51	7.6	705	6	US-10-703-032-60562	Sequence 60562, A
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8	47.2	7.0	696	13	US-11-053-052-18	Sequence 18, Appl

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20 47.2 7.0 553 21 46.8 6.9 17437 23 46.6 6.9 17433 24 46.6 6.9 12164 25 46.6 6.9 2964 27 46.6 6.9 2964 27 46.6 6.9 2964 27 46.7 6.9 1216 28 46.2 6.9 673 30 46.2 6.9 673 31 46.2 6.9 673 34 46 6.8 1739 36 46 6.8 1739 37 46 6.8 1739 38 46 6.8 3752 39 46 6.8 3753 39 46 6.8 3754 40 6.8 3754 41 46 6.8 3754 42 45.8 6.8 4773 44 45.8 6.8 4773 45 6.8 5283 46 6.8 3754 4773 47 46 6.8 3754 48 4773 49 45.8 6.8 4773	- B	Þ	60-669-241- 11-031-175- 11-097-143- 11-097-143-	11-031-175-7 11-100-356-5 11-100-356-1	55555	11-100-356-5 11-100-356-5 11-100-356-1 11-031-175-9 11-031-175-9
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ALIGNMENTS

US-60-680-544-44583 Sequence 44583, Application US/60680544	; GENERAL INFORMATION: ; APPLICANT: Cooper, Matthew ; applicant: Kinch Deborah	Rosenberg, Micha	: Szak, Suzanne			NVENTION: Nucleotide Array Containing Polynucleotide	; TITLE OF INVENTION: Fragments of, Cynomolgus Monkey Genes and the Use Thereof	; CURRENT APPLICATION NUMBER: US/60/680,544	; CURRENT FILING DATE: 2005-05-13	. NUMBER OF SEL IN NOS: 2017.	SEO ID NO 44583	; LENGTH: 2302	, 112F LUNA ; ORGANISM: Homo Sapiens US-60-680-544-44583		19.6%; Score 516.2; DB 15; Dength 2502; Similarity 88.2%; Pred. No. 7.3e-90;	583; Conservative 0; Mismatches 78; Indels 0; Gaps	Oy 14 CCTTCCTCCTTCTGGCACCATGCCACTAGCCCCTTGCCTTGCCTGCTTGT 73	Db 29 CCTCCTCTCGCTGGTACCATGCAGCTCCCACTGGCCCTGTCTCGCCTGCTGGTGT 88	Oy 74 ACATGCAGCCTTCGTTGCTGTGGAGCCAGGGTGGCAAGCCTTCAAGAATGATGCCAC 133	Db 89 ACACACAGCCTTCCGTGTAGTGGAGGCCCAGGGGTGGCAGGCGTTCAAGAATGATGCCAC 148	Oy 134 AGADATCATCCCGGGACTCAGAGAGTACCCAGAGCCTCCTCAGGAACTAGAGAACAACCA 193	149 CZSBBBTCETCTCGBGCTCGGBGGCTCCGGGGGGGCTGCGAGCBACCBACCBACCBACCAACCAACCAACCAACCAA
Ty, Matthew h. Deborah	nberg, Wichael amaniam, S. Sai amaniam, S. Sai amaniam, S. Sai amaniam, S. Sai and Sai aru, Raj aru, Raj con: Nucleotide Array Containing Polynucleotide ON: Presgmente of, Cynomolgus Monkey Genes and ION NUMBER: US/60/680,544 ATE: 2005-05-13 NOS: 48714 ATE: 2005-0	Augustume, 3. 321. Huo aru, Raj aru, R	Huo aru, Raj aru, Raj aru, Raj aru, Raj on: Nucleotide Array Containing Polymucleotide ON: Nucleotide Array Containing Polymucleotide ON: Nucleotide Array Containing Polymucleotide ON: Pragments of, Cynomolgus Monkey Genes and ION NUMBER: US/60/680,544 ATE: 2005-05-13 A	aru, kaal aru, kaal aru, kaal aru, kaal and array Containing Polynucleotide ON: Pregmente of, Cynomolgus Monkey Genes and 10N: Pregmente of, Cynomolgus Monkey Genes and 10N: NUMBER: US/60/680,544 ATS: 2005-05-13 NOS: 48714 ATS: 2005-05-13 NOS: 48714 ATS: 2005-05-13 Sapiens 79.6%; Score 536.2; DB 15; Length 230 rity 88.2%; Pred. No. 7.38-90; CTCTTCGGCTGGCGCTCTCACTGGCCTTGCCTGCCTGCCT	ON: Nucleotide Array Containing Polymucleotide ON: Fragments of, Cynomolgus Monkey Genes and 1018 POLYMERS: US/60/680,544 ATE: 2005-05-13 NOS: 48714 ATE: 2005-05-13 NOS: 48714 Sequence Analysis Tool Version 1.0 Sequence Analysis Tool Version 1.0 Ty. 6%; Score 536.2; DB 15; Length 230 rity 88.2%; Pred: No. 7.38-90; CTCTTCTGGCTGGTGCTTGCTTGCTTGCTTGCTTGCTTG	ON: Fragments of, Cynomolgus Monkey Genes and 21590290000 21590290000 21590290000 31590290000 31590290000 31590290000 3159029000 3159029000 3159029000 3159029000 315902902 3159029020 3159029020 3159029020 3159029020 31590290290 3159029020 31590200000000000000000000000000000000000	100 NUMBER: US/60/680,544	######################################	Sequence Analysis Tool Version 1.0 Sequence Analysis Tool Version 1.0 rity 88.2%; Score 536.2; DB 15; Length 2302; rity 88.2%; Pred. No. 7.38-90; nservative 0; Mismatches 78; Indels 0; Gaps crccrrcaccaccarccaccaccaccaccarccaracccaracaraccaracaracaraccaracaracaracaraccaracaraccaracar	Sapiens 79.6%; Score 536.2; DB 15; Length 2302; rity 88.2%; Pred. No. 7.3e-90; nservative 0; Mismatches 78; Indels 0; Gaps crccrrcracacacaracacacacacacacacacacaca	19.6%; Score 536.2; DB 15; Length 2302; It 88.2%; Pred. No. 7.38-90; nservative	Sapiens rity 88.2%; Score 536.2; DB 15; Length 2302; miscrative 0; Mismatches 78; Indels 0; Gaps crectroredcaccarecaercreareaeccorrectrectrer 73	Duery Match 19.6%; Score 536.2; DB 15; Length 2302; 4atches 583; Conservative 0; Mismatches 78; Indels 0; Gaps 14 CCTTCCTTCTGGCACCATGCAGCTCTCACTAGCCCTTGCTTG	15 15 15 15 15 15 15 15	<pre>datches 583; Conservative 0; Mismatches 78; Indels 0; Gaps 14 CCTTCCTCTTCTGGCACCATGCAGCTCTCACTAGCCCTTGCCTGCC</pre>	14 CCTTCCTCTTCTGGCACCATGCAGCTCACTAGCCCTTGCCTTGCCTGCTTGT 29 CCCTCCTCTGGCAGCTGCAGCTCCCAGGCCCTGGCTTGCTT	29 CCCTCCTGGCTGGTACTTGCTGCTGCTGGCCCTGGTGCTCTGGCTGG	74 ACATGCAGCCTTCGTTGCTGTGGAGGCCAGGGGTGGCAGGCTTCAAGAATGATGCCAC	89 ACACAGCCTTCCGTGTAGTGGAGGCCAGGGGTGGCAGGCGTTCAAGAATGATGCCAC 134 AGAAATCATCCCGGGACTCGAGAGTAGTACCCAGGGGTTCCTCCTCGGAACTAGAGAACAACCA 149 GGAAATCATCCCCGAGCTCGGAAGTACCCCGAGCTCCACGGAGCTGGAAACAA	134 AGANATCATCCCGGGACTCAGAGAGTACCCAGAGCCTCCTCAGGAACTAGAGAACCACCAGAGCTCCACCGGAAACAACAACAACAACAACAACAACAACAACAA	149 GGAAATCATCCCGGAGTTCGGAGAGTACCCCGGAGCTCCACCGGAGCTCGAGAAACAACAA	

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US-09-668-021-9 US-09-668-021-9 US-09-668-529A-45 US-09-668-037A-45 US-09-668-037A-15 US-09-668-037A-15 US-09-668-031A-15 US-09-449-218D-17 US-09-449-218D-17 US-09-668-037A-17 US-09-668-037A-17 US-09-668-037A-18 US-09-668-037A-18 US-09-668-037A-18	US-09-688-021-18 US-09-513-999C-9816 US-09-188-930-40
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RESULT 1
US-09-449-218D-13
US-09-449-218D-13
Sequence 13, Application US/09449218D
Fatent No. 6395511
GENERAL INFORMATION:
FAPPLICANT: Brunkow, Mary E.
FAPPLICANT: Brunkow, Mary E.
FAPPLICANT: Wordcevich, Brian
FAPPLICANT: Wordcevich, Brian
FAPPLICANT: Wan Ness, Jeffrey
FAPPLICANT: Wan Ness, Jeffrey
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
TITLE OF INVENTION: BONE MINERALIZATION
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: 1999-11-24
TITLE OF INVENTION: 1999-11-24
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEG for Windows Version 3.0
SEQ ID NO 13
ERNGTH: 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 674; DB 3; Length 674;
Best Local Similarity 100.0%; Pred. No. 9.7e-149;
Matches 674; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Rattus norvegicus
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	version 5.1.6 - 2005 Compugen Ltd.	
OM nucleic - nucleic search, using sw model	w model	
Run on: June 28, 2005, 14:54:42	June 28, 2005, 14:54:42 ; Search time 2399.78 Seconds (without alignments) 10741.894 Million cell updates/sec	

1 agaatgacacagaaatc.....accaaagccagccgggccga 532 4708233 segs, 24227607955 residues Total number of hits satisfying chosen parameters: IDENTITY NUC Gapop 10.0 , Gapext 1.0 US-10-788-606-15 532 Title: Perfect score: Scoring table: Sequence: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Compositi Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence AF326738 Bos tauru Sequence Ното варі Compositi Sequence Sequence Sequence Description AR259025 AR267698 AR267698 AR321698 AR321693 AR321653 AR32165 BD2551906 AR258992 AR267166 AR267166 AR371666 AR3 BD251913 AR258999 AR267472 AR371672 SUMMARIES AR267466 AR371665 AR371666 Length DB Query Score 467.8 467.8 Result No.

AF326739 Homo sapi	AX056687 Sequence	AX574536 Sequence	AY358627 Homo sapi	BD251908 Compositi	BD251909 Compositi	AR258994 Sequence	AR258995 Sequence	AR267467 Sequence	AR267468 Sequence				AR258996 Sequence	AR267469 Seguence	AR371669 Sequence	AF326742 Cercopith	BD251912 Compositi	AR258998 Sequence	AR267471 Sequence	AR371671 Sequence	AF326741 Rattus no	AY358203 Homo sapi	AX323455 Sequence	BD251911 Compositi	AR258997 Seguence
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87.9	87.9	87.9	87.9	87.6	87.6	87.6	87.6	87.6	87.6	87.6	87.6	86.7	86.7	86.7	86.7	86.7	79.8	79.8	79.8	79.8	79.8	79.6	78.2	77.9	77.9
467.8	467.8	467.8	467.8	466.2	466.2	466.2	466.2	466.2	466.2	466.2	466.2	461.4	461.4	461.4	461.4	461.4	424.6	424.6	424.6	424.6	424.6	423.4	415.8	414.2	414.2

ALIGNMENTS

AF326738 532 bp mRNA linear MAM 28-FEB-2001 Bos taurus sclerostin mRNA, partial cds. AF326738.1 GI:13161016	Bos taurus Bos taurus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	<pre>1 (bases 1 to 532) Brunkow,M.E., Gardner,J.C., Van Ness,J., Paeper,B.W., Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J., Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., Galas,D., Hamersma,H. Beighton,P. and Mulligan,J.T.</pre>	Done dysplain Scientedels Frencis from loss of the Sosi gene product, a novel cystine knot-containing protein Am. J. Hum. Genet. 68 (3), 577-589 (2001) 21090529 11179066 Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W., Kovaecvich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J., Hanersma, H., Beighton, P. and Mulligan, J.T.	Direct Submission Submitted (Or-DEC-2000) Genomics, Celltech Chiroscience Inc., 1631 220th St. SE, Bothell, WA 98021, USA Location/Qualifiers 1. 532 /organism="Bos taurus" & /mol type="mRNA" /db_xref="taxon:9913"	<pre><1>532 /codon_gtart=3 /product="sclerostin" /procein_id="AAK13453.1" /db_xref="01:13161017" /translation="NDATELIFELGEYPEPLPELNNKTWARAENGGRPPHHPFETKDA</pre>
RESULT 1 AF326738 LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL MEDLINE PUBNED REFERENCE AUTHORS	TITLE JOURNAL FEATURES SOUICE	CDS

SEYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWWRPSGPDFR

score:

Perfect

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

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AY400962 642 bp DNA linear GSS 15-DEC-2003
Homo gapiens SOST gene, VIRTUAL TRANSCRIPT, partial sequence,
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Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Homo sapiens
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Database :

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ï 9 1 AGAATGGTGCCACAGAATCATCCCCGAGCTGGGCGAGTACCCCGAGCCTCTGCCAGAGC Сарв 3, 87.9%; Score 467.8; DB 9; Length 642; 93.5%; Pred. No. 1.6e-90; Live 0; Mismatches 32; Indels 3 organism="Homo sapiens" |mol_type="genomic DNA" |db_xref="taxon:9606" /gene="SOST" /locus_tag="HCM0732" Location/Qualifiers Query Match
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AY400963 BE101082 AF184211 BX282099 AI556282 BB638050 AI11313131

Result

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6/ptodata'1/pubpna/US09 NWW PUB.seq:*
6/ptodata'1/pubpna/US10A PUBCOMB.seq:*
6/ptodata'1/pubpna/US10B_PUBCOMB.seq:*
6/ptodata'1/pubpna/US10C_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/DCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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ptodata/1/pubpna/US10H_PUBCOMB.seq:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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44: ⟨cgn2 6/ptodata/1/pna/US099F COMB. seq: *
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60: ⟨cgn2 6/ptodata/1/pna/US6002 COMB. seq: *
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2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
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		99, Appl	44583, A	14583, A	23752, A	23752, A	, Appli	9087, Ap	1072, Ap	7231, Ap	577, App	48429, A	18429, A	7216, Ap	24312, A	1241, Ap	8735, A	•	977, App
	Description	Sequence 99, Appl	Sequence 44583,	Sequence 44583,	Sequence 23752,	Sequence 23752,	Sequence 1, Appli	Sequence 9087,	Sequence	Sequence 7231,	Sequence 677, App	Sequence 48429,	Sequence 48429	Seguence	Sequence 24312,	Sequence	Sequence 28735,	Sequence 3318	Sequence 977,
SUMMARIES		US-60-677-583-99	US-60-680-544-44583	US-60-680-473-44583	US-60-680-544-23752	-60-680-473-23752	-US05-13260-1	-11-031-175-9087	-11-031-175-1072	-11-031-175-7231	US-11-031-175-677	-60-680-544-48429	US-60-680-473-48429	US-60-669-175-7216	US-60-669-241-24312	US-11-031-175-1241	10-703-032-28735	-11-031-175-3318	US-11-031-175-977
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87.9%; Score 467.8; DB 15; Length 570;
Best Local Similarity 93.5%; Pred. No. 5.7e-70;
Matches 500; Conservative 0; Mismatches 32; Indels 3;
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5: /cgn2_6/ptodatea1/ina/FB_COMB.seq:*
6: /cgn2_6/ptodatea1/ina/PCTUS COMB.seq:*
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ALIGNMENTS

GENERAL INFORMATION:
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APPLICANT: Mulligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Van Ness, Jeffrey
APPLICANT: Winkler, David G.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
ITILE OF INVENTION: BONE MINERALIZATION
TITLE OF INVENTION: UNDER MINERALIZATION
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE PASESEQ for Windows Version 3.0
: SEQ ID NO 15
LENGTH: 532 Sequence 15, Application US/09449218D Patent No. 6395511 US-09-449-218D-15

TYPE: DNA ORGANISM: Bos torus US-09-449-218D-15

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